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## RAW SEQUENCE LISTING

DATE: 11/28/2001

PATENT APPLICATION: US/09/921,650B

TIME: 18:10:13

Input Set : A:\09921650A.raw.txt

Output Set: N:\CRF3\11212001\I921650B.raw

## SEQUENCE LISTING

ENTERED

## 1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Bujard, Hermann  
3 Gossen, Manfred

4 (ii) TITLE OF INVENTION: Tetracycline-Inducible Transcriptional  
5 Inhibitor Fusion Proteins

6 (iii) NUMBER OF SEQUENCES: 37

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: LAHIVE & COCKFIELD

9 (B) STREET: 28 State Street

10 (C) CITY: Boston

11 (D) STATE: Massachusetts

12 (E) COUNTRY: USA

13 (F) ZIP: 02109-1875

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk

16 (B) COMPUTER: IBM PC compatible

17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

18 (D) SOFTWARE: ASCII Text

19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/09/921,650B

C--> 21 (B) FILING DATE: 03-Aug-2001

22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:

24 (A) APPLICATION NUMBER: US/09/489,777

25 (B) FILING DATE: 24-Jan-2000

26 (A) APPLICATION NUMBER: US 09/162,184

27 (B) FILING DATE: 28-SEP-1998

28 (A) APPLICATION NUMBER: US 08/485,978

29 (B) FILING DATE: 07-JUN-1995

30 (A) APPLICATION NUMBER: US 08/383,754

31 (B) FILING DATE: 03-FEB-1995

32 (A) APPLICATION NUMBER: US 08/275,876

33 (B) FILING DATE: 15-JULY-1994

34 (A) APPLICATION NUMBER: US 08/270,637

35 (B) FILING DATE: 01-JULY-1994

36 (A) APPLICATION NUMBER: US 08/260,452

37 (B) FILING DATE: 14-JUNE-1994

38 (A) APPLICATION NUMBER: US 08/076,327

39 (B) FILING DATE: 14-JUNE-1993

40 (A) APPLICATION NUMBER: US 08/076,726

41 (B) FILING DATE: 14-JUNE-1993

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: DeConti, Giulio A. Jr.

44 (B) REGISTRATION NUMBER: 31,503

45 (C) REFERENCE/DOCKET NUMBER: BBI-009C6CNDV

46 (ix) TELECOMMUNICATION INFORMATION:

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47      (A) TELEPHONE: (617)227-7400
48      (B) TELEFAX: (617)742-4214
49 (2) INFORMATION FOR SEQ ID NO: 1:
50      (i) SEQUENCE CHARACTERISTICS:
51          (A) LENGTH: 1008 base pairs
52          (B) TYPE: nucleic acid
53          (C) STRANDEDNESS: double
54          (D) TOPOLOGY: linear
W--> 55      (ii) MOLECULE TYPE: DNA
56      (ix) FEATURE:
57          (A) NAME/KEY: exon
58          (B) LOCATION: 1..1008
59      (ix) FEATURE:
60          (A) NAME/KEY: mRNA
61          (B) LOCATION: 1..1008
62      (ix) FEATURE:
63          (A) NAME/KEY: misc. binding
64          (B) LOCATION: 1..207
65      (ix) FEATURE:
66          (A) NAME/KEY: misc. binding
67          (B) LOCATION: 208..335
68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION: 1..1005
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72      ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG      48
73      Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
74      1          5          10          15
75      CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG      96
76      Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
77      20          25          30
78      AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG      144
79      Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
80      35          40          45
81      CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT      192
82      Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
83      50          55          60
84      ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC      240
85      Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
86      65          70          75          80
87      AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA      288
88      Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
89      85          90          95
90      GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT      336
91      Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
92      100          105          110
93      CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG      384
94      Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
95      115          120          125

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96  AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC      432
97  Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
98      130                      135                      140
99  GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA      480
100  Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
101      145                      150                      155                      160
102  CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA      528
103  Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
104                      165                      170                      175
105  TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG      576
106  Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
107                      180                      185                      190
108  ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG      624
109  Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
110                      195                      200                      205
111  TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC      672
112  Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
113      210                      215                      220
114  CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG      720
115  Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
116      225                      230                      235                      240
117  GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG      768
118  Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
119                      245                      250                      255
120  ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC      816
121  Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
122                      260                      265                      270
123  GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT      864
124  Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
125                      275                      280                      285
126  CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC      912
127  Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
128      290                      295                      300
129  CAC GAC TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT      960
130  His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
131      305                      310                      315                      320
132  GAG CAG ATG TTT ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG      1008
133  Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
134                      325                      330                      335

136 (2) INFORMATION FOR SEQ ID NO: 2:
137   (i) SEQUENCE CHARACTERISTICS:
138       (A) LENGTH: 335 amino acids
139       (B) TYPE: amino acid
140       (D) TOPOLOGY: linear
141   (ii) MOLECULE TYPE: protein
142   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
143   Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
144       1             5             10             15
145   Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln

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146		20		25		30	
147	Lys	Leu	Gly	Val	Glu	Gln	Pro
148		35		40		45	
149	Arg	Ala	Leu	Leu	Asp	Ala	Leu
150		50		55		60	
151	Thr	His	Phe	Cys	Pro	Leu	Lys
152		65		70		75	
153	Asn	Lys	Ala	Lys	Ser	Phe	Arg
154			85			90	
155	Ala	Lys	Val	His	Ser	Asp	Thr
156		100				105	
157	Leu	Glu	Asn	Gln	Leu	Ala	Phe
158		115				120	
159	Asn	Ala	Leu	Tyr	Ala	Leu	Ser
160		130				135	
161	Val	Leu	Glu	Asp	Gln	Glu	His
162		145				150	
163	Pro	Thr	Thr	Asp	Ser	Met	Pro
164				165			170
165	Phe	Asp	His	Gln	Gly	Ala	Glu
166			180				185
167	Ile	Ile	Cys	Gly	Leu	Glu	Lys
168		195					200
169	Tyr	Ser	Arg	Ala	Arg	Thr	Lys
170		210					215
171	Leu	Leu	Asp	Leu	Pro	Asp	Asp
172		225					230
173	Ala	Pro	Arg	Leu	Ser	Phe	Leu
174			245				250
175	Thr	Ala	Pro	Pro	Thr	Asp	Val
176			260				265
177	Gly	Glu	Asp	Val	Ala	Met	Ala
178		275					280
179	Leu	Asp	Met	Leu	Gly	Asp	Gly
180		290					295
181	His	Asp	Ser	Ala	Pro	Tyr	Gly
182		305					310
183	Glu	Gln	Met	Phe	Thr	Asp	Pro
184			325				330

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG 33

Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu

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196          1          5          10
198 (2) INFORMATION FOR SEQ ID NO: 4:
199     (i) SEQUENCE CHARACTERISTICS:
200         (A) LENGTH: 11 amino acids
201         (B) TYPE: amino acid
202         (D) TOPOLOGY: linear
203     (ii) MOLECULE TYPE: peptide
204     (v) FRAGMENT TYPE: internal
205     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
206         Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
207         1          5          10
209 (2) INFORMATION FOR SEQ ID NO: 5:
210     (i) SEQUENCE CHARACTERISTICS:
211         (A) LENGTH: 7 amino acids
212         (B) TYPE: amino acid
213         (D) TOPOLOGY: linear
214     (ii) MOLECULE TYPE: peptide
215     (v) FRAGMENT TYPE: internal
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
217         Met Pro Lys Arg Pro Arg Pro
218         1          5
220 (2) INFORMATION FOR SEQ ID NO: 6:
221     (i) SEQUENCE CHARACTERISTICS:
222         (A) LENGTH: 569 base pairs
223         (B) TYPE: nucleic acid
224         (C) STRANDEDNESS: double
225         (D) TOPOLOGY: linear
W--> 226     (ii) MOLECULE TYPE: DNA
227     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
228         GAATTCGGGG CCGCGGAGGC TGGATCGGTC CCGGTGTCTT CTATGGAGGT CAAAACAGCG      60
229         TGGATGGCGT CTCCAGGCGA TCTGACGGTT CACTAAACGA GCTCTGCTTA TATAGGTCGA      120
230         GTTTACCAGT CCCTATCAGT GATAGAGAAA AGTGAAAGTC GAGTTTACCA CTCCCTATCA      180
231         GTGATAGAGA AAAGTGAAAG TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA      240
232         AGTCGAGTTT ACCACTCCCT ACCAGTGATA GAGAAAAGTG AAAGTCGAGT TTACCACTCC      300
233         CTATCAGTGA TAGAGAAAAG TGAAAGTCGA GTTTACCACT CCCTATCAGT GATAGAGAAA      360
234         AGTGAAAGTC GAGTTTACCA CTCCCTATCA GTGATAGAGA AAAGTGAAAG TCGAGCTCGG      420
235         TACCCGGGTC GAGTAGGCGT GTACGGTGGG AGGCCTATAT AAGCAGAGCT CGTTTAGTGA      480
236         ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTTGA CCTCCATAGA AGACACCGGG      540
237         ACCGATCCAG CCTCCGCGGC CCCGAATTC      569
239 (2) INFORMATION FOR SEQ ID NO: 7:
240     (i) SEQUENCE CHARACTERISTICS:
241         (A) LENGTH: 520 base pairs
242         (B) TYPE: nucleic acid
243         (C) STRANDEDNESS: double
244         (D) TOPOLOGY: linear
W--> 245     (ii) MOLECULE TYPE: DNA
246     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
247         AGATCTGCAG GGTGCTCGG TGTTGAGGC CACACGCGTC ACCTTAATAT GCGAAGTGGA      60
248         CCGGATCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC      120

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## VERIFICATION SUMMARY

DATE: 11/28/2001

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TIME: 18:10:14

Input Set : A:\09921650A.raw.txt

Output Set: N:\CRF3\11212001\I921650B.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1  
L:192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3  
L:226 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:245 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:328 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11  
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12  
L:348 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13  
L:358 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14  
L:368 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15  
L:681 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24  
L:691 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25  
L:712 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27